

09831765.054101

GGGGCCACGG	GGGGTGCGCC	GGCGCGCGGT	AGCGCGGGCC	CCTCAGTGCA	CAATGGCCAG	60
AGCAGGCGGC	GGAGCCCCAG	CCCCACCCAG	TGCGGAGCGC	GCCGCGAGCC	CCGCCGCAAG	120
CTGAGCGCCT	CCGCCCGCCA	GGCGCGCCGG	CGCCGGGCCA	TGTACTCGGG	GAACCGCAGC	180
GGCGGCCACG	GCTACTGGGA	CGGCGCGCGG	GCCGCGGGCG	CTGAGGGGCC	GGCGCCGGCG	240
GGGACACTGA	GCCCCGCGCC	CCTCTTCAGC	CCCGGCACCT	ACGAGCGCCT	GGCGCTGCTG	300
CTGGGCTCCA	TTGGGCTGCT	GGGCGTCGGC	AACAACCTGC	TGGTGCTCGT	CCTCTACTAC	360
AAGTTCCAGC	GGCTCCGCAC	TCCCACTCAC	CTCCTCCTGG	TCAACATCAG	CCTCAGCGAC	420
CTGCTGGTGT	CCCTCTTCGG	GGTCACCTTT	ACCTTCGTGT	CCTGCCTGAG	GAACGGCTGG	480
GTGTGGGACA	CCGTGGGCTG	CGTGTGGGAC	GGGTTTAGCG	GCAGCCTCTT	CGGGATTGTT	540
TCCATTGCCA	CCCTAACCGT	GCTGGCCTAT	GAACGTTACA	TTGCGGTGGT	CCATGCCAGA	600
GTGATCAATT	TTTCTGGGCG	CTGGAGGGCC	ATTACCTACA	TCTGGCTCTA	CTCACTGGCG	660
TGGGCAGGAG	CACCTCTCCT	GGGATGGAAC	AGGTACATCC	TGGACGTACA	CGGACTAGGC	720
TGCACTGTGG	ACTGGAATC	CAAGGATGCC	AACGATTCTT	CCTTTGTGCT	TTTCTTATTT	780
CTTGGCTGCC	TGGTGGTGCC	CCTGGGTGTC	ATAGCCCAT	GCTATGGCCA	TATTCTATAT	840
TCCATTCCAA	TGCTTCGTTG	TGTGGAAGAT	CTTCAGACAA	TTCAAGTGAT	CAAGATTTTA	900
AAATATGAAA	AGAAACTGGC	CAAAATGTGC	TTTTTAATGA	TATTCACCTT	CCTGGTCTGT	960
TGGATGCCTT	ATATCGTGAT	CTGCTTCTTG	GTGGTTAATG	GTCATGGTCA	CCTGGTCACT	1020
CCAACAATAT	CTATTGTTTC	GTACCTCTTT	GCTAAATCGA	ACACTGTATA	CAATCCAGTG	1080
ATTTATGTCT	TCATGATCAG	AAAGTTTCGA	AGATCCCTTT	TGCAGCTTCT	GTGCCTCCGA	1140
CTGCTGAGGT	GCCAGAGGCC	TGCTAAAGAC	CTACCAGCAG	CTGGAAGTGA	AATGCAGATC	1200
AGACCCATTG	TGATGTCACA	GAAAGATGGG	GACAGGCCAA	AGAAAAAAGT	GACTTTCAAC	1260
TCTTCTTCCA	TCATTTTTAT	CATCACCAGT	GATGAATCAC	TGTCAGTTGA	CGACAGCGAC	1320
AAAACCAATG	GGTCCAAAGT	TGATGTAATC	CAAGTTCTGC	CTTTGTAGGA	ATGAAGAATG	1380
GCAACGAAAG	ATGGGGCCTT	AAATTGGATG	CCACTTTTGG	ACTTTTCATCA	TAAGAAGTGT	1440
CTGGAATACC	CGTTCTATGT	AATATCAACA	GAACCTTGTG	GTCCAGCAGG	AAATCCGAAT	1500
TGCCCATATG	CTCTTGGGCC	TCAGGAAGAG	GTTGAAC	(SEQ ID NO:1)		1537

FIG.1

1 MYSGNRSGGH GYWDGGAAG AEGPAPAGTL SPAPLFSPGT YERLALLGS
51 IGLLGVGNNL LVLVLYYKFQ RLRTPTHLL VNISLSDLLV SLFGVTFTFV
101 SCLRNGWWD TVGCWWDGFS GSLEGIWSIA TLTVLAYERY IRVWHARVIN
151 FSWAWRAITY IWLYSLAWAG APLLGWNYI LDVHGLGCTV DWKSKDANDS
201 SFVLFLFLGC LVVPLGVIAH CYGHILYSIR MLRCVEDLQT IQVIKILKYE
251 KKLAKMCFLM IFTFLVCWMP YIVICFLVN GHGHLVTPTI SIVSYLFAKS
301 NTVYNPVIYV FMIRKFRRSL LQLLCLRLR CQPAKDLPA AGSEMQIRPI
351 VMSQKGDGRP KKKVTFNSSS IIFIITSDES LSVDDSDKTN GSKVDVIQVR
401 PL (SEQ ID NO:2)

FIG.2

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GGGGCCACGG GGGGTGCGCC GGCGGCGCGT AGCGCGGGCC CCTCAGTGCA CAATGGCCAG 60
 AGCAGGCGGC GGAGCCCCAG CCCCACCCAG TGCGGAGCGC GCGCGAGCC CCGCGCAAG 120
 CTGAGCGCCT CCGCCGCCA GGCGGCGCGG CGCGGGCC ATG TAC TCG GGG AAC 174
 MET TYR SER GLY ASN
 1 5

CGC AGC GGC GGC CAC GGC TAC TGG GAC GGC GGC GGG GCC GCG GGC GCT 222
 ARG SER GLY GLY HIS GLY TYR TRP ASP GLY GLY GLY ALA ALA GLY ALA
 10 15 20

GAG GGC CCG GCG CCG GCG GGG ACA CTG AGC CCC GCG CCC CTC TTC AGC 270
 GLU GLY PRO ALA PRO ALA GLY THR LEU SER PRO ALA PRO LEU PHE SER
 25 30 35

CCC GGC ACC TAC GAG CGC CTG GCG CTG CTG CTG GGC TCC ATT GGG CTG 318
 PRO GLY THR TYR GLU ARG LEU ALA LEU LEU LEU GLY SER ILE GLY LEU
 40 45 50

CTG GGC GTC GGC AAC AAC CTG CTG GTG CTC GTC CTC TAC TAC AAG TTC 366
 LEU GLY VAL GLY ASN ASN LEU LEU VAL LEU VAL LEU TYR TYR LYS PHE
 55 60 65

CAG CGC CTC CGC ACT CCC ACT CAC CTC CTC CTG GTC AAC ATC AGC CTC 414
 GLN ARG LEU ARG THR PRO THR HIS LEU LEU LEU VAL ASN ILE SER LEU
 70 75 80 85

AGC GAC CTG CTG GTG TCC CTC TTC GGG GTC ACC TTT ACC TTC GTG TCC 462
 SER ASP LEU LEU VAL SER LEU PHE GLY VAL THR PHE THR PHE VAL SER
 90 95 100

TGC CTG AGG AAC GGC TGG GTG TGG GAC ACC GTG GGC TGC GTG TGG GAC 510
 CYS LEU ARG ASN GLY TRP VAL TRP ASP THR VAL GLY CYS VAL TRP ASP
 105 110 115

GGG TTT AGC GGC AGC CTC TTC GGG ATT GTT TCC ATT GCC ACC CTA ACC 558
 GLY PHE SER GLY SER LEU PHE GLY ILE VAL SER ILE ALA THR LEU THR
 120 125 130

GTG CTG GCC TAT GAA CGT TAC ATT CGC GTG GTC CAT GCC AGA GTG ATC 606
 VAL LEU ALA TYR GLU ARG TYR ILE ARG VAL VAL HIS ALA ARG VAL ILE
 135 140 145

FIG. 3A

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AAT TTT TCC TGG GCC TGG AGG GCC ATT ACC TAC ATC TGG CTC TAC TCA ASN PHE SER TRP ALA TRP ARG ALA ILE THR TYR ILE TRP LEU TYR SER 150 155 160 165	654
CTG GCG TGG GCA GGA GCA CCT CTC CTG GGA TGG AAC AGG TAC ATC CTG LEU ALA TRP ALA GLY ALA PRO LEU LEU GLY TRP ASN ARG TYR ILE LEU 170 175 180	702
GAC GTA CAC GGA CTA GGC TGC ACT GTG GAC TGG AAA TCC AAG GAT GCC ASP VAL HIS GLY LEU GLY CYS THR VAL ASP TRP LYS SER LYS ASP ALA 185 190 195	750
AAC GAT TCC TCC TTT GTG CTT TTC TTA TTT CTT GGC TGC CTG GTG GTG ASN ASP SER SER PHE VAL LEU PHE LEU PHE LEU GLY CYS LEU VAL VAL 200 205 210	798
CCC CTG GGT GTC ATA GCC CAT TGC TAT GGC CAT ATT CTA TAT TCC ATT PRO LEU GLY VAL ILE ALA HIS CYS TYR GLY HIS ILE LEU TYR SER ILE 215 220 225	846
CGA ATG CTT CGT TGT GTG GAA GAT CTT CAG ACA ATT CAA GTG ATC AAG ARG MET LEU ARG CYS VAL GLU ASP LEU GLN THR ILE GLN VAL ILE LYS 230 235 240 245	894
ATT TTA AAA TAT GAA AAG AAA CTG GCC AAA ATG TGC TTT TTA ATG ATA ILE LEU LYS TYR GLU LYS LYS LEU ALA LYS MET CYS PHE LEU MET ILE 250 255 260	942
TTC ACC TTC CTG GTC TGT TGG ATG CCT TAT ATC GTG ATC TGC TTC TTG PHE THR PHE LEU VAL CYS TRP MET PRO TYR ILE VAL ILE CYS PHE LEU 265 270 275	990
GTG GTT AAT GGT CAT GGT CAC CTG GTC ACT CCA ACA ATA TCT ATT GTT VAL VAL ASN GLY HIS GLY HIS LEU VAL THR PRO THR ILE SER ILE VAL 280 285 290	1038
TCG TAC CTC TTT GCT AAA TCG AAC ACT GTA TAC AAT CCA GTG ATT TAT SER TYR LEU PHE ALA LYS SER ASN THR VAL TYR ASN PRO VAL ILE TYR 295 300 305	1086
GTC TTC ATG ATC AGA AAG TTT CGA AGA TCC CTT TTG CAG CTT CTG TGC VAL PHE MET ILE ARG LYS PHE ARG ARG SER LEU LEU GLN LEU LEU CYS 310 315 320 325	1134

FIG. 3B

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CTC CGA CTG CTG AGG TGC CAG AGG CCT GCT AAA GAC CTA CCA GCA GCT 1182
 LEU ARG LEU LEU ARG CYS GLN ARG PRO ALA LYS ASP LEU PRO ALA ALA
 330 335 340

GGA AGT GAA ATG CAG ATC AGA CCC ATT GTG ATG TCA CAG AAA GAT GGG 1230
 GLY SER GLU MET GLN ILE ARG PRO ILE VAL MET SER GLN LYS ASP GLY
 345 350 355

GAC AGG CCA AAG AAA AAA GTG ACT TTC AAC TCT TCT TCC ATC ATT TTT 1278
 ASP ARG PRO LYS LYS LYS VAL THR PHE ASN SER SER SER ILE ILE PHE
 360 365 370

ATC ATC ACC AGT GAT GAA TCA CTG TCA GTT GAC GAC AGC GAC AAA ACC 1326
 ILE ILE THR SER ASP GLU SER LEU SER VAL ASP ASP SER ASP LYS THR
 375 380 385

AAT GGG TCC AAA GTT GAT GTA ATC CAA GTT CGT CCT TTG TAGGAATGAA 1375
 ASN GLY SER LYS VAL ASP VAL ILE GLN VAL ARG PRO LEU (SEQ ID NO:2)
 390 395 400

GAATGGCAAC GAAAGATGGG GCCTTAAATT GGATGCCACT TTTGGACTTT CATCATAAGA 1435
 AGTGTCTGGA ATACCCGTTT TATGTAATAT CAACAGAACC TTGTGGTCCA GCAGGAAATC 1495
 CGAATTGCCC ATATGCTCTT GGGCCTCAGG AAGAGGTTGA AC (SEQ ID NO:2) 1537

FIG. 3C

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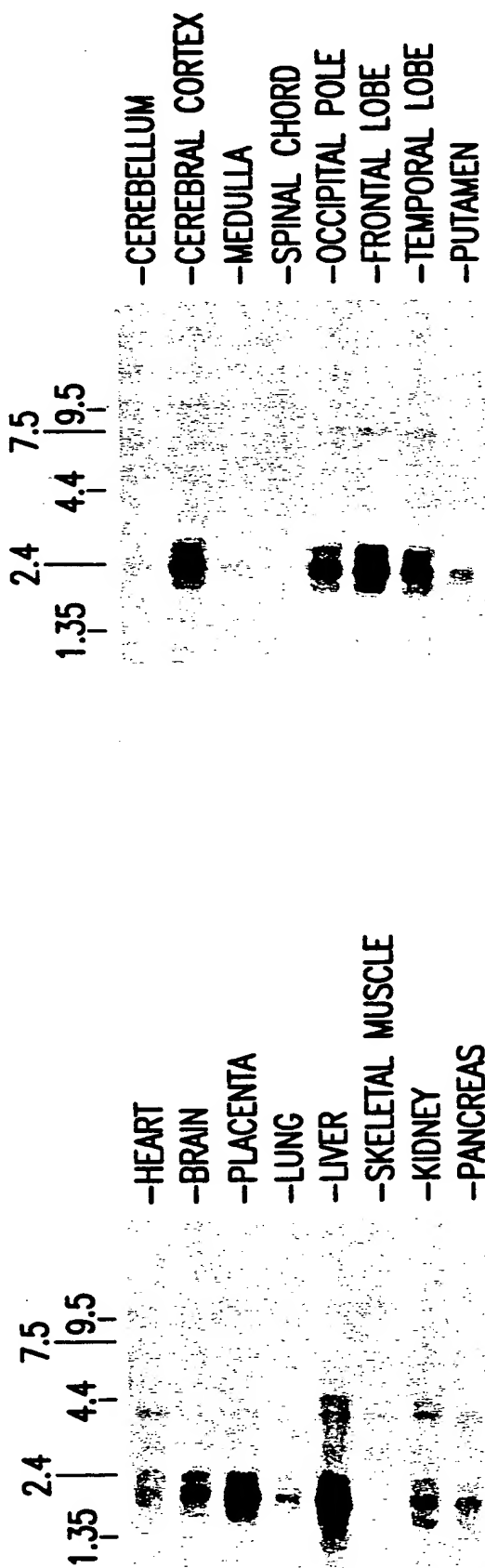


FIG.4A

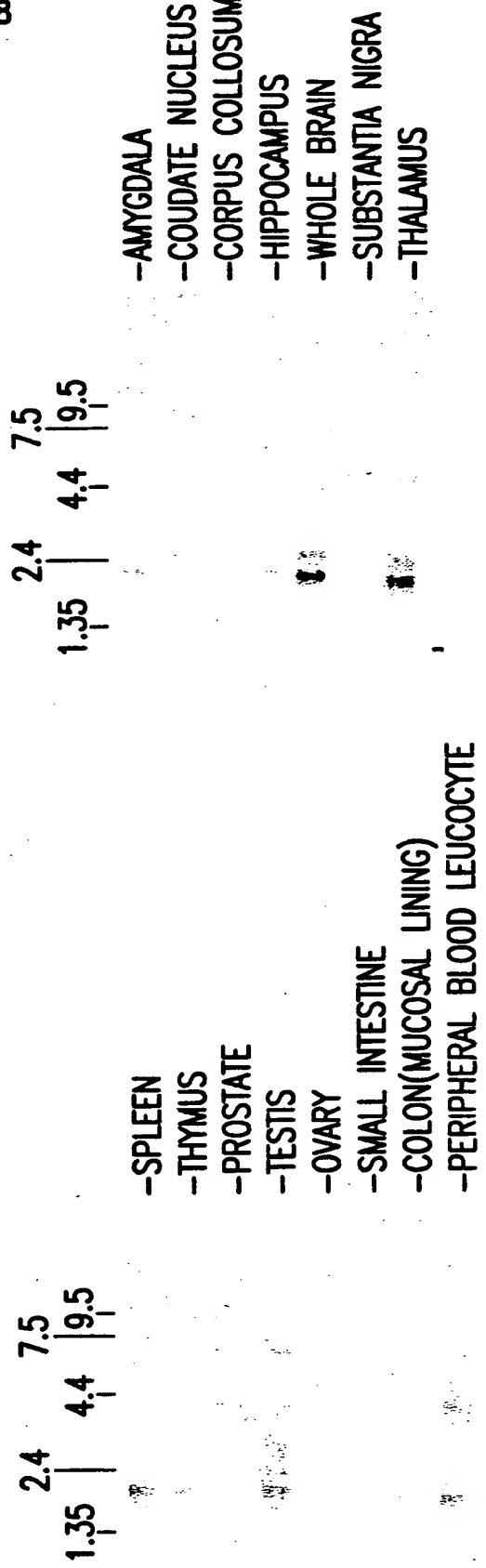


FIG.4B

FIG.4C

FIG.4D

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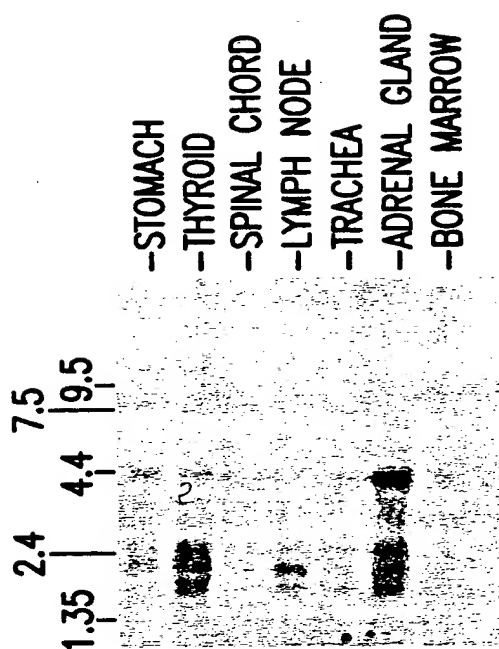


FIG.4E

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	10	20	30	40	50	60
RHODOPSIN	MNGTEGPNFYVPFSNATGVVRSPFEYPOYYLAEPWQFSMLAAYMFLIVLGFPINFLTLY					
				I I : II : : II I:I:I		
HG51	NRSGGHGYWDGGAAGAECPAPAGTLPAPLFSPTGYERLALLGSLGLGVGNLLVLV					
	10	20	30	40	50	60

	70	80	90	100	110	120
RHODOPSIN	VTVQHKKLRTPLNILLNLAVADLFMVLGGFTSTLYTSLHGYFVFGPTGCNLEGGFFATLG					
	: : : IIII : : I : : I : : I : : I : : I : : I : : I : : I : : I					
HG51	LYYKFQRLRTPHLLLVNISLSDLLVSLFGVTFVVSCLRNGWVMDTVGCVWDGFGSGLF					
	70	80	90	100	110	120

	130	140	150	160	170	179
RHODOPSIN	GEIALWSLVLAIERV-VVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLAGWSRYI					
	I : : : I : IIII III : II : II : I : : : I : : I : I : I : I : IIII					
HG51	GIVSIATLTVLAYERYIRVVHARVINFSW----AWRAITYIWL YSLAWAGAPLLGWNRYI					
	130	140	150	160	170	180

	180	190	200	210	220	230
RHODOPSIN	PEGLQCSCGIDYYTLKPEVNNEFVIYMFVHFTIPMIIFFCYGQLVFTVKEAAA----					
	: : I : : : : : I : : I : : I : : I : : I : : I : : I : : I : : I					
HG51	LDVHGLGCTVDWKS--KDANDSSFVLFLLGLVPLGVIAHCYGHILYSIRMLRCVEDL					
	190	200	210	220	230	

	240	250	260	270	280	290
RHODOPSIN	QQQESATTQAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTIPAFFA					
	I : : I III : : I : : I : : I : : I : : I : : I : : I : : I : : I					
HG51	QTIQVIKILKYEKKLAKMCFMIFTFLVCMMPYIVICFLVNGHGHVLTPTISIVSYLFA					
	240	250	260	270	280	290

	300	310	320	330	340
RHODOPSIN	KSAAIYNPVIYIMMINKQFRNCMLTTICGKNPLGDEASATVSKTETSQVAPA (SEQ ID NO:15)				
	II : : IIII : : I : : I : : I : : I : : I : : I : : I : : I : : I				
HG51	KSNTVYNPVIYVFMIRKFRSLLQLLCLRLRCQRPAPKDLPAAGSEMQRPIVMSQKDG				
	300	310	320	330	340
					350
					(CONTAINED WITHIN SEQ. ID NO:2)

FIG. 5

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